

RESULT 1

BCDO\_CHICK

ID BCDO\_CHICK STANDARD; PRT; 526 AA.  
AC Q9I993;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Beta,beta-carotene 15,15'-dioxygenase (EC 1.14.99.36) (Beta-carotene  
DE dioxygenase 1).  
GN BCDO.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN=LSL Lohmann; TISSUE=Duodenum;  
RX MEDLINE=20261261; PubMed=10799297;  
RA Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,  
RA Bachmann H., Hunziker W.;  
RT "Cloning and expression of beta,beta-carotene-15,15'-dioxygenase.";  
RL Biochem. Biophys. Res. Commun. 271:334-336(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LSL Lohmann; TISSUE=Duodenum;  
RX MEDLINE=21134366; PubMed=11237856;  
RA Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,  
RA Riss G., Bachmann H., Hunziker W.;  
RT "Expression pattern and localization of beta,beta-carotene 15,15'-  
RT dioxygenase in different tissues.";  
RL Biochem. J. 354:521-529(2001).  
CC -!- FUNCTION: Symmetrically cleaves beta-carotene into two molecules  
CC of retinal. The reaction proceeds in three stages, epoxidation of  
CC the 15,15'-double bond, hydration of the double bond leading to  
CC ring opening, and oxidative cleavage of the diol formed.  
CC -!- CATALYTIC ACTIVITY: Beta-carotene + O(2) = 2 retinal.  
CC -!- COFACTOR: Iron.  
CC -!- PATHWAY: Vitamin A biosynthesis.  
CC -!- SIMILARITY: Belongs to the beta-carotene dioxygenase family.  
CC -----  
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CC -----  
DR EMBL; AJ271386; CAB90825.1; -.  
DR InterPro; IPR004294; RPE65.  
DR Pfam; PF03055; RPE65; 1.  
KW Dioxygenase; Oxidoreductase; Iron.  
SQ SEQUENCE 526 AA; 60384 MW; 82C6EAAF75FE345B CRC64;

Query Match 100.0%; Score 2825; DB 1; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.4e-191;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60
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Db      1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60

Qy     61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDCKNIFAKAFSYLSHTIPEF 120
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Db     61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDCKNIFAKAFSYLSHTIPEF 120

Qy    121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180
      |||
Db    121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180

Qy    181 ILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCIPSRSLLQPSYYHSFGI 240
      |||
Db    181 ILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCIPSRSLLQPSYYHSFGI 240

Qy    241 TENYIVFIEQPFKLDIVKLATAYIRGVNWSCLSFHKEDKTWFHFVDRKTKKEVSTKFYT 300
      |||
Db    241 TENYIVFIEQPFKLDIVKLATAYIRGVNWSCLSFHKEDKTWFHFVDRKTKKEVSTKFYT 300

Qy    301 DALVLYHHINAYEEDGHVVFDDIVAYRDNSLYDMFYLLKKLDKDFEVNNKLTSIPTCKRFVV 360
      |||
Db    301 DALVLYHHINAYEEDGHVVFDDIVAYRDNSLYDMFYLLKKLDKDFEVNNKLTSIPTCKRFVV 360

Qy    361 PLQYDKDAEVGSNLVKLPTSATAVKEKDGSIIYQPEILCEGIELPRVNYDYGKKYKYVY 420
      |||
Db    361 PLQYDKDAEVGSNLVKLPTSATAVKEKDGSIIYQPEILCEGIELPRVNYDYGKKYKYVY 420

Qy    421 ATEVQWSPVPTKIAKLVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCTVVVSE 480
      |||
Db    421 ATEVQWSPVPTKIAKLVQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCTVVVSE 480

Qy    481 PNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFIPQNDLGAETE 526
      |||
Db    481 PNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFIPQNDLGAETE 526
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RESULT 1

Q7ZTS0

ID Q7ZTS0 PRELIMINARY; PRT; 516 AA.  
AC Q7ZTS0;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Bcdol protein.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Body;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Body;  
RA Strausberg R.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC049331; AAH49331.1; -.  
DR InterPro; IPR004294; RPE65.  
DR Pfam; PF03055; RPE65; 1.  
SQ SEQUENCE 516 AA; 58655 MW; DFBAC7D058736E53 CRC64;

Query Match 60.9%; Score 1720; DB 13; Length 516;  
Best Local Similarity 59.9%; Pred. No. 3.7e-123;  
Matches 311; Conservative 86; Mismatches 114; Indels 8; Gaps 5;

Qy 1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWF DGLALLHSF 60  
| : : : ||||| ||| :| :| :| ||| :| :| ||||| :| :| ||||| :| :|  
Db 1 MQDYDGKNKEEHPEPIKTEVKGSIP EWVQGT LIRNGPGMFSVGETTYNHWF DGMALLHSF 60  
Qy 61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVSEFGT MAYPD PCKNIFAKAFSYLSHTIPEF 120  
||| ||| :||| |||| :| :| ||||| ||||| ||||| ||||| :| :| ||||| :|

Db 61 AINKGEVTYRSRYLRGDTYNSNMQANRIVVSEMGTMAYPDCKNIFSKVITFLSHTIPDF 120  
 Qy 121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180  
 |||| |::| |:::|||||:||||| |||| :|::| ||: |:: || ||| ||  
 Db 121 TDNCGNNIIKYGNDFHATSETNYIRKIDPVTLETQEKIDYLYLPVSIVASHTHYDKEGN 180  
 Qy 181 ILNMGTSIVDKGRTKYVLFKIP-SSVPEKEKKKSCFKHLEVVCIPSRSLLQPSYYHSFG 239  
 :||| |:::||||:||||: | | : | |::| |||| |||||  
 Db 181 SYSMGTICIAEKGKTKYMLFKVPGESRPDGSP---LKSAEAVCTLPCRSLTTPSYHSFG 237  
 Qy 240 ITENYIVFIEQPFLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFY 299  
 :|::| :||| ||||:|:||||:| |::|: || || | :|| |||||:||||  
 Db 238 MTDNYFIFIEQPLKLDILKMATAYLRRVSWASCMKFHPEDSTLIHLIDRNTKKEVATKFY 297  
 Qy 300 TDALVLYHHINAYEEDGHVVFDIVAYRDNLSLYDMFYLLKKLDKDFEVNNKLTSIPTCKRFV 359  
 |||: :|| :||:|:|||||:|:| ||:|: ||| || : | | | ||  
 Db 298 TDAMTVYHQVNAFEDDGHVVFDVIAYDDNNLYEFFYLNKLKETMGATN-LYCKPKFTRFV 356  
 Qy 360 VPLQYDKDAEVGSNLVKLP-TSATAVKEKDGSICYQPEILCEGIELPRVNYDYNKKYKY 418  
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 Db 357 FPL--SDQGETGENLVKLKYTTASAVKEKDGMKIMCQGEVLCEGVLPRIYNFNKKYRY 414  
 Qy 419 VYATEVQWSPVPTKIAKLVNQTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTVCVVV 478  
 | | ||| |:| | : ||: : | | : |||:|:| | | :||:|||| ::  
 Db 415 SYMCCVDESPVATRIVKFDADTKQIEWKGGDFASEPVFIPRPGAVDEDDGVVLTVIIN 474  
 Qy 479 SEPNAKAPLLILDAKTFKELGRATVNVEMHLDLHGMFIP 517  
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 Db 475 NKPLQGGFLLVLDKSFKEIARACLDVEIHMDMHGYFIP 513